

SEQUENCE LISTING

(I) GENERAL INFORMATION:

(i) APPLICANT: University of Pittsburgh of the Commonwealth System
of Higher Education, 911 William Pitt Union
Pittsburgh, PA 15260

(ii) TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue
of a Mammalian Host

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Eckert Seamans Cherin & Mellott, LLC
(B) STREET: 600 Grant Street, 42nd Floor
(C) CITY: Pittsburgh
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 15219

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Meyers, Diane R.
(B) REGISTRATION NUMBER: 38,968
(C) REFERENCE/DOCKET NUMBER: 109070-11-1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (412) 566-6000
(B) TELEFAX: (412) 566-6099
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1770 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human T-cell cDNA Library
- (B) CLONE: Human Interleukin-1 Receptor

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 55..1764

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTCCTGAGA AGCTGGACCC CTTGGTAAAA GACAAGGCCT TCTCCAAGAA GAAT ATG	57
	Met
	1
AAA GTG TTA CTC AGA CTT ATT TGT TTC ATA GCT CTA CTG ATT TCT TCT	105
Lys Val Leu Leu Arg Leu Ile Cys Phe Ile Ala Leu Leu Ile Ser Ser	
	5 10 15
CTG GAG GCT GAT AAA TGC AAG GAA CGT GAA GAA AAA ATA ATT TTA GTG	153
Leu Glu Ala Asp Lys Cys Lys Arg Glu Glu Lys Ile Ile Leu Val	
	20 25 30
TCA TCT GCA AAT GAA ATT GAT GTT CGT CCC TGT CCT CTT AAC CCA AAT	201
Ser Ser Ala Asn Glu Ile Asp Val Arg Pro Cys Pro Leu Asn Pro Asn	
	35 40 45
GAA CAC AAA GGC ACT ATA ACT TGG TAT AAA GAT GAC AGC AAG ACA CCT	249
Glu His Lys Gly Thr Ile Thr Trp Tyr Lys Asp Asp Ser Lys Thr Pro	
	50 55 60 65
GTA TCT ACA GAA CAA GCC TCC AGG ATT CAT CAA CAC AAA GAG AAA CTT	297
Val Ser Thr Glu Gln Ala Ser Arg Ile His Gln His Lys Glu Lys Leu	
	70 75 80
TGG TTT GTT CCT GCT AAG GTG GAG GAT TCA GGA CAT TAC TAT TGC GTG	345
Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly His Tyr Tyr Cys Val	
	85 90 95
GTA AGA AAT TCA TCT TAC TGC CTC AGA ATT AAA ATA AGT GCA AAA TTT	393
Val Arg Asn Ser Ser Tyr Cys Leu Arg Ile Lys Ile Ser Ala Lys Phe	
	100 105 110

GAG Val	GAG Glu 115	AAT Asn	GAG Glu	CCT Pro	AAC Asn	TTA Leu 120	TGT Cys	TAT Tyr	AAT Asn	GCA Ala	CAA Gln 125	GCC Ala	ATA Ile	TTT Phe	AAG Lys	441
CAG Gln 130	AAA Lys	CTA Leu	CCC Pro	GTT Val	GCA Ala 135	GGA Gly	GAC Asp	GGA Gly	GGA Gly	CTT Leu 140	GTG Val	TGC Cys	CCT Pro	TAT Tyr	ATG Met 145	489
GAG Glu	TTT Phe	TTT Phe	AAA Lys	AAT Asn 150	GAA Glu	AAT Asn	AAT Asn	GAG Glu	TTA Leu 155	CCT Pro	AAA Lys	TTA Leu	CAG Gln	TGG Trp 160	TAT Tyr	537
AAG Lys	GAT Asp	TGC Cys	AAA Lys 165	CCT Pro	CTA Leu	CTT Leu	CTT Leu	GAC Asp 170	AAT Asn	ATA Ile	CAC His	TTT Phe	AGT Ser 175	GGA Gly	GTC Val	585
AAA Lys	GAT Asp	AGG Arg 180	CTC Leu	ATC Ile	GTG Val	ATG Met	AAT Asn 185	GTG Val	GCT Ala	GAA Glu	AAG Lys	CAT His 190	AGA Arg	GGG Gly	AAC Asn	633
TAT Tyr	ACT Thr 195	TGT Cys	CAT His	GCA Ala	TCC Ser	TAC Tyr 200	ACA Thr	TAC Tyr	TTG Leu	GGC Gly 205	AAG Lys	CAA Gln	TAT Tyr	CCT Pro	ATT Ile	681
ACC Thr 210	CGG Arg	GTA Val	ATA Ile	GAA Glu	TTT Phe 215	ATT Ile	ACT Thr	CTA Leu	GAG Glu 220	GAA Glu	AAC Asn	AAA Lys	CCC Pro	ACA Thr	AGG Arg 225	729
CCT Pro	GTG Val	ATT Ile	GTG Val	AGC Ser 230	CCA Pro	GCT Ala	AAT Asn	GAG Glu	ACA Thr 235	ATG Met	GAA Glu	GTA Val	GAC Asp	TTG Leu 240	GGA Gly	777
TCC Ser	CAG Gln	ATA Ile	CAA Gln 245	TTG Leu	ATC Ile	TGT Cys	AAT Asn	GTC Val 250	ACC Thr	GGC Gly	CAG Gln	TTG Leu	AGT Ser 255	GAC Asp	ATT Ile	825
GCT Ala	TAC Tyr	TGG Trp 260	AAG Lys	TGG Trp	AAT Asn	GGG Gly	TCA Ser 265	GTA Val	ATT Ile	GAT Asp	GAA Glu	GAT Asp 270	GAC Asp	CCA Pro	GTG Val	873
CTA Leu	GGG Gly 275	GAA Glu	GAC Asp	TAT Tyr	TAC Tyr	AGT Ser 280	GTG Val	GAA Glu	AAT Asn	CCT Pro	GCA Ala 285	AAC Asn	AAA Lys	AGA Arg	AGG Arg	921
AGT Ser 290	ACC Thr	CTC Leu	ATC Ile	ACA Thr	GTG Val 295	CTT Leu	AAT Asn	ATA Ile	TCG Ser	GAA Glu 300	ATT Ile	GAA Glu	AGT Ser	AGA Arg	TTT Phe 305	969
TAT Tyr	AAA Lys	CAT His	CCA Pro	TTT Phe 310	ACC Thr	TGT Cys	TTT Phe	GCC Ala	AAG Lys 315	AAT Asn	ACA Thr	CAT His	GGT Gly	ATA Ile 320	GAT Asp	1017
GCA Ala	GCA Ala	TAT Tyr	ATC Ile 325	CAG Gln	TTA Leu	ATA Ile	TAT Tyr	CCA Pro 330	GTC Val	ACT Thr	AAT Asn	TTC Phe	CAG Gln 335	AAG Lys	CAC His	1065
ATG Met	ATT Ile	GGT Gly 340	ATA Ile	TGT Cys	GTC Val	ACG Thr	TTG Leu 345	ACA Thr	GTC Val	ATA Ile	ATT Ile	GTG Val 350	TGT Cys	TCT Ser	GTT Val	1113
TTC Phe	ATC Ile 355	TAT Tyr	AAA Lys	ATC Ile	TTC Phe	AAG Lys 360	ATT Ile	GAC Asp	ATT Ile	GTG Val	CTT Leu 365	TGG Trp	TAC Tyr	AGG Arg	GAT Asp	1161
TCC Ser 370	TGC Cys	TAT Tyr	GAT Asp	TTT Phe	CTC Leu 375	CCA Pro	ATA Ile	AAA Lys	GCT Ala	TCA Ser 380	GAT Asp	GGA Gly	AAG Lys	ACC Thr	TAT Tyr 385	1209

GAC	GCA	TAT	ATA	CTG	TAT	CCA	AAG	ACT	GTT	GGG	GAA	GGG	TCT	ACC	TCT	1257
Asp	Ala	Tyr	Ile	Leu	Tyr	Pro	Lys	Thr	Val	Gly	Glu	Gly	Ser	Thr	Ser	
				390					395					400		
GAC	TGT	GAT	ATT	TTT	GTG	TTT	AAA	GTC	TTG	CCT	GAG	GTC	TTG	GAA	AAA	1305
Asp	Cys	Asp	Ile	Phe	Val	Phe	Lys	Val	Leu	Pro	Glu	Val	Leu	Glu	Lys	
			405					410					415			
CAG	TGT	GGA	TAT	AAG	CTG	TTC	ATT	TAT	GGA	AGG	GAT	GAC	TAC	GTT	GGG	1353
Gln	Cys	Gly	Tyr	Lys	Leu	Phe	Ile	Tyr	Gly	Arg	Asp	Asp	Tyr	Val	Gly	
		420					425					430				
GAA	GAC	ATT	GTT	GAG	GTC	ATT	AAT	GAA	AAC	GTA	AAG	AAA	AGC	AGA	AGA	1401
Glu	Asp	Ile	Val	Glu	Val	Ile	Asn	Glu	Asn	Val	Lys	Lys	Ser	Arg	Arg	
	435					440					445					
CTG	ATT	ATC	ATT	TTA	GTC	AGA	GAA	ACA	TCA	GGC	TTC	AGC	TGG	CTG	GGT	1449
Leu	Ile	Ile	Ile	Leu	Val	Arg	Glu	Thr	Ser	Gly	Phe	Ser	Trp	Leu	Gly	
450					455					460				465		
GGT	TCA	TCT	GAA	GAG	CAA	ATA	GCC	ATG	TAT	AAT	GCT	CTT	GTT	CAG	GAT	1497
Gly	Ser	Ser	Glu	Glu	Gln	Ile	Ala	Met	Tyr	Asn	Ala	Leu	Val	Gln	Asp	
			470						475					480		
GGA	ATT	AAA	GTT	GTC	CTG	CTT	GAG	CTG	GAG	AAA	ATC	CAA	GAC	TAT	GAG	1545
Gly	Ile	Lys	Val	Val	Leu	Leu	Glu	Leu	Glu	Lys	Ile	Gln	Asp	Tyr	Glu	
			485					490					495			
AAA	ATG	CCA	GAA	TCG	ATT	AAA	TTC	ATT	AAG	CAG	AAA	CAT	GGG	GCT	ATC	1593
Lys	Met	Pro	Glu	Ser	Ile	Lys	Phe	Ile	Lys	Gln	Lys	His	Gly	Ala	Ile	
		500					505					510				
CGC	TGG	TCA	GGG	GAC	TTT	ACA	CAG	GGA	CCA	CAG	TCT	GCA	AAG	ACA	AGG	1641
Arg	Trp	Ser	Gly	Asp	Phe	Thr	Gln	Gly	Pro	Gln	Ser	Ala	Lys	Thr	Arg	
	515					520					525					
TTC	TGG	AAG	AAT	GTC	AGG	TAC	CAC	ATG	CCA	GTC	CAG	CGA	CGG	TCA	CCT	1689
Phe	Trp	Lys	Asn	Val	Arg	Tyr	His	Met	Pro	Val	Gln	Arg	Arg	Ser	Pro	
530				535						540				545		
TCA	TCT	AAA	CAC	CAG	TTA	CTG	TCA	CCA	GCC	ACT	AAG	GAG	AAA	CTG	CAA	1737
Ser	Ser	Lys	His	Gln	Leu	Leu	Ser	Pro	Ala	Thr	Lys	Glu	Lys	Leu	Gln	
			550					555						560		
AGA	GAG	GCT	CAC	GTG	CCT	CTC	GGG	TAGCATGGA								1770
Arg	Glu	Ala	His	Val	Pro	Leu	Gly									
			565				570									

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Val Leu Leu Arg Leu Ile Cys Phe Ile Ala Leu Leu Ile Ser
 1 5 10 15

Val Leu Gly Glu Asp Tyr Tyr Ser Val Glu Asn Pro Ala Asn Lys Arg
275 280 285

Pro Ser Ser Lys His Gln Leu Leu Ser Pro Ala Thr Lys Glu Lys Leu
545 550 555 560

Gln Arg Glu Ala His Val Pro Leu Gly
565

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1782 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Mouse T-cell cDNA Library
- (B) CLONE: Mouse Interleukin-1 Receptor

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..1776

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
GGATGTCATC AGAGTTCCCA GTGCCCCGAA CCGTGAACAA CACAA ATG GAG AAT      54
                                         Met Glu Asn
                                         1

ATG AAA GTG CTA CTG GGG CTC ATT TGT CTC ATG GTG CCT CTG CTG TCG      102
Met Lys Val Leu Leu Gly Leu Ile Cys Leu Met Val Pro Leu Leu Ser
      5                      10                      15

CTG GAG ATT GAC GTA TGT ACA GAA TAT CCA AAT CAG ATC GTT TTG TTT      150
Leu Glu Ile Asp Val Cys Thr Glu Tyr Pro Asn Gln Ile Val Leu Phe
      20                      25                      30                      35

TTA TCT GTA AAT GAA ATT GAT ATT CGC AAG TGT CCT CTT ACT CCA AAT      198
Leu Ser Val Asn Glu Ile Asp Ile Arg Lys Cys Pro Leu Thr Pro Asn
                      40                      45                      50

AAA ATG CAC GGC GAC ACC ATA ATT TGG TAC AAG AAT GAC AGC AAG ACC      246
Lys Met His Gly Asp Thr Ile Ile Trp Tyr Lys Asn Asp Ser Lys Thr
                      55                      60                      65

CCC ATA TCA GCG GAC CGG GAC TCC AGG ATT CAT CAG CAG AAT GAA CAT      294
Pro Ile Ser Ala Asp Arg Asp Ser Arg Ile His Gln Gln Asn Glu His
      70                      75                      80
```

CTT Leu	TGG Trp 85	TTT Phe	GTA Val	CCT Pro	GCC Ala	AAG Lys 90	GTG Val	GAG Glu	GAC Asp	TCA Ser	GGA Gly 95	TAT Tyr	TAC Tyr	TAT Tyr	TGT Cys	342
ATA Ile 100	GTA Val	AGA Arg	AAC Asn	TCA Ser	ACT Thr 105	TAC Tyr	TGC Cys	CTC Leu	AAA Lys	ACT Thr 110	AAA Lys	GTA Val	ACC Thr	GTA Val	ACT Thr 115	390
GTG Val	TTA Leu	GAG Glu	AAT Asn 120	GAC Asp 120	CCT Pro	GGC Gly	TTG Leu	TGT Cys	TAC Tyr 125	AGC Ser	ACA Thr	CAG Gln	GCC Ala	ACC Thr 130	TTC Phe	438
CCA Pro	CAG Gln	CGG Arg	CTC Leu 135	CAC His	ATT Ile	GCC Ala	GGG Gly	GAT Asp 140	GGA Gly	AGT Ser	CTT Leu	GTG Val 145	TGC Cys 145	CCT Pro	TAT Tyr	486
GTG Val	AGT Ser	TAT Tyr 150	TTT Phe	AAA Lys	GAT Asp	GAA Glu	AAT Asn 155	AAT Asn	GAG Glu	TTA Leu	CCC Pro	GAG Glu 160	GTC Val	CAG Gln	TGG Trp	534
TAT Tyr	AAG Lys 165	AAC Asn	TGT Cys	AAA Lys	CCT Pro	CTG Leu 170	CTT Leu	CTT Leu	GAC Asp	AAC Asn	GTG Val 175	AGC Ser	TTC Phe	TTC Phe	GGA Gly	582
GTA Val 180	AAA Lys	GAT Asp	AAA Lys	CTG Leu 185	TTG Leu 185	GTG Val	AGG Arg	AAT Asn	GTG Val 190	GCT Ala 190	GAA Glu	GAG Glu	CAC His	AGA Arg	GGG Gly 195	630
GAC Asp	TAT Tyr	ATA Ile	TGC Cys	CGT Arg 200	ATG Met	TCC Ser	TAT Tyr	ACG Thr	TTC Phe 205	CGG Arg	GGG Gly	AAG Lys	CAA Gln	TAT Tyr 210	CCG Pro	678
GTC Val	ACA Thr	CGA Arg	GTA Val 215	ATA Ile	CAA Gln	TTT Phe	ATC Ile	ACA Thr 220	ATA Ile	GAT Asp	GAA Glu	AAC Asn	AAG Lys 225	AGG Arg	GAC Asp	726
AGA Arg	CCT Pro	GTT Val 230	ATC Ile	CTG Leu	AGC Ser	CCT Pro	CGG Arg 235	AAT Asn	GAG Glu	ACG Thr	ATC Ile 240	GAA Glu 240	GCT Ala	GAC Asp	CCA Pro	774
GGA Gly	TCA Ser 245	ATG Met	ATA Ile	CAA Gln	CTG Leu	ATC Ile 250	TGC Cys	AAC Asn	GTC Val	ACG Thr	GGC Gly 255	CAG Gln	TTC Phe	TCA Ser	GAC Asp	822
CTT Leu 260	GTC Val	TAC Tyr	TGG Trp	AAG Lys	TGG Trp 265	AAT Asn	GGA Gly	TCA Ser	GAA Glu	ATT Ile 270	GAA Glu	TGG Trp	AAT Asn	GAT Asp	CCA Pro 275	870
TTT Phe	CTA Leu	GCT Ala	GAA Glu	GAC Asp 280	TAT Tyr	CAA Gln	TTT Phe	GTG Val	GAA Glu 285	CAT His	CCT Pro	TCA Ser	ACC Thr	AAA Lys 290	AGA Arg	918
AAA Lys	TAC Tyr	ACA Thr	CTC Leu 295	ATT Ile	ACA Thr	ACA Thr	CTT Leu 300	AAC Asn	ATT Ile	TCA Ser	GAA Glu	GTT Val	AAA Lys 305	AGC Ser	CAG Gln	966
TTT Phe	TAT Tyr	CGC Arg 310	TAT Tyr	CCG Pro	TTT Phe	ATC Ile	TGT Cys 315	GTT Val	GTT Val	AAG Lys	AAC Asn	ACA Thr 320	AAT Asn	ATT Ile	TTT Phe	1014
GAC Glu	TCG Ser 325	GCG Ala	CAT His	GTG Val	CAG Gln	TTA Leu 330	ATA Ile	TAC Tyr	CCA Pro	GTC Val	CCT Pro 335	GAC Asp	TTC Phe	AAG Lys	AAT Asn	1062
TAC Tyr 340	CTC Leu	ATC Ile	GGG Gly	GGC Gly	TTT Phe 345	ATC Ile	ATC Ile	CTC Leu	ACG Thr	GCT Ala 350	ACA Thr	ATT Ile	GTA Val	TGC Cys	TGT Cys 355	1110

GTG	TGC	ATC	TAT	AAA	GTC	TTC	AAG	GTT	GAC	ATA	GTG	CTT	TGG	TAC	AGG	1158
Val	Cys	Ile	Tyr	Lys	Val	Phe	Lys	Val	Asp	Ile	Val	Leu	Trp	Tyr	Arg	
				360					365					370		
GAC	TCC	TGC	TCT	GGT	TTT	CTT	CCT	TCA	AAA	GCT	TCA	GAT	GGA	AAG	ACA	1206
Asp	Ser	Cys	Ser	Gly	Phe	Leu	Pro	Ser	Lys	Ala	Ser	Asp	Gly	Lys	Thr	
			375					380					385			
TAC	GAT	GCA	TAT	ATT	CTT	TAT	CCC	AAG	ACC	CTG	GGA	GAG	GGG	TCC	TTC	1254
Tyr	Asp	Ala	Tyr	Ile	Leu	Tyr	Pro	Lys	Thr	Leu	Gly	Glu	Gly	Ser	Phe	
		390					395					400				
TCA	GAC	TTA	GAT	ACT	TTT	GTT	TTT	AAA	CTG	TTG	CCT	GAG	GTC	TTG	GAG	1302
Ser	Asp	Leu	Asp	Thr	Phe	Val	Phe	Lys	Leu	Leu	Pro	Glu	Val	Leu	Glu	
	405					410					415					
GGA	CAG	TTT	GGA	TAC	AAG	CTG	TTC	ATT	TAT	GGA	AGG	GAT	GAC	TAT	GTT	1350
Gly	Gln	Phe	Gly	Tyr	Lys	Leu	Phe	Ile	Tyr	Gly	Arg	Asp	Asp	Tyr	Val	
420					425					430					435	
GGA	GAA	GAT	ACC	ATC	GAG	GTT	ACT	AAT	GAA	AAT	GTA	AAG	AAA	AGC	AGG	1398
Gly	Glu	Asp	Thr	Ile	Glu	Val	Thr	Asn	Glu	Asn	Val	Lys	Lys	Ser	Arg	
				440				445						450		
AGG	CTG	ATT	ATC	ATT	CTA	GTG	AGA	GAT	ATG	GGA	GGC	TTC	AGC	TGG	CTG	1446
Arg	Leu	Ile	Ile	Ile	Leu	Val	Arg	Asp	Met	Gly	Gly	Phe	Ser	Trp	Leu	
			455					460					465			
GGC	CAG	TCA	TCT	GAA	GAG	CAA	ATA	GCC	ATA	TAC	AAT	GCT	CTC	ATC	CAG	1494
Gly	Gln	Ser	Ser	Glu	Glu	Gln	Ile	Ala	Ile	Tyr	Asn	Ala	Leu	Ile	Gln	
		470					475					480				
GAA	GGA	ATT	AAA	ATC	GTC	CTG	CTT	GAG	TTG	GAG	AAA	ATC	CAA	GAC	TAT	1542
Glu	Gly	Ile	Lys	Ile	Val	Leu	Leu	Glu	Leu	Glu	Lys	Ile	Gln	Asp	Tyr	
	485					490					495					
GAG	AAA	ATG	CCA	GAT	TCT	ATT	CAG	TTC	ATT	AAG	CAG	AAA	CAC	GGA	GTC	1590
Glu	Lys	Met	Pro	Asp	Ser	Ile	Gln	Phe	Ile	Lys	Gln	Lys	His	Gly	Val	
500					505					510					515	
ATT	TGC	TGG	TCA	GGA	GAC	TTT	CAA	GAA	AGA	CCA	CAG	TCT	GCA	AAG	ACC	1638
Ile	Cys	Trp	Ser	Gly	Asp	Phe	Gln	Glu	Arg	Pro	Gln	Ser	Ala	Lys	Thr	
				520					525					530		
AGG	TTC	TGG	AAA	AAC	TTA	AGA	TAC	CAG	ATG	CCA	GCC	CAA	CGG	AGA	TCA	1686
Arg	Phe	Trp	Lys	Asn	Leu	Arg	Tyr	Gln	Met	Pro	Ala	Gln	Arg	Arg	Ser	
			535					540					545			
CCA	TTG	TCT	AAA	CAC	CGC	TTA	CTA	ACC	CTG	GAT	CCT	GTG	CGG	GAC	ACT	1734
Pro	Leu	Ser	Lys	His	Arg	Leu	Leu	Thr	Leu	Asp	Pro	Val	Arg	Asp	Thr	
		550					555					560				
AAG	GAG	AAA	CTG	CCG	GCA	GCA	ACA	CAC	TTA	CCA	CTC	GGC	TAGCATGGC			1782
Lys	Glu	Lys	Leu	Pro	Ala	Ala	Thr	His	Leu	Pro	Leu	Gly				
	565					570					575					

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

093435 130500

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Asn Met Lys Val Leu Leu Gly Leu Ile Cys Leu Met Val Pro
1 5 10 15

Leu Leu Ser Leu Glu Ile Asp Val Cys Thr Glu Tyr Pro Asn Gln Ile
20 25 30

Val Leu Phe Leu Ser Val Asn Glu Ile Asp Ile Arg Lys Cys Pro Leu
35 40 45

Thr Pro Asn Lys Met His Gly Asp Thr Ile Ile Trp Tyr Lys Asn Asp
50 55 60

Ser Lys Thr Pro Ile Ser Ala Asp Arg Asp Ser Arg Ile His Gln Gln
65 70 75 80

Asn Glu His Leu Trp Phe Val Pro Ala Lys Val Glu Asp Ser Gly Tyr
85 90 95

Tyr Tyr Cys Ile Val Arg Asn Ser Thr Tyr Cys Leu Lys Thr Lys Val
100 105 110

Thr Val Thr Val Leu Glu Asn Asp Pro Gly Leu Cys Tyr Ser Thr Gln
115 120 125

Ala Thr Phe Pro Gln Arg Leu His Ile Ala Gly Asp Gly Ser Leu Val
130 135 140

Cys Pro Tyr Val Ser Tyr Phe Lys Asp Glu Asn Asn Glu Leu Pro Glu
145 150 155 160

Val Gln Trp Tyr Lys Asn Cys Lys Pro Leu Leu Leu Asp Asn Val Ser
165 170 175

Phe Phe Gly Val Lys Asp Lys Leu Leu Val Arg Asn Val Ala Glu Glu
180 185 190

His Arg Gly Asp Tyr Ile Cys Arg Met Ser Tyr Thr Phe Arg Gly Lys
195 200 205

Gln Tyr Pro Val Thr Arg Val Ile Gln Phe Ile Thr Ile Asp Glu Asn
210 215 220

Lys Arg Asp Arg Pro Val Ile Leu Ser Pro Arg Asn Glu Thr Ile Glu
225 230 235 240

Ala Asp Pro Gly Ser Met Ile Gln Leu Ile Cys Asn Val Thr Gly Gln
245 250 255

His Gly Val Ile Cys Trp Ser Gly Asp Phe Gln Glu Arg Pro Gln Ser
515 520 525

Ala Lys Thr Arg Phe Trp Lys Asn Leu Arg Tyr Gln Met Pro Ala Gln
530 535 540

Arg Arg Ser Pro Leu Ser Lys His Arg Leu Leu Thr Leu Asp^{*}Pro Val
545 550 555 560

Arg Asp Thr Lys Glu Lys Leu Pro Ala Ala Thr His Leu Pro Leu Gly
565 570 575

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Primer Oligonucleotide to 5'Leader Sequence of
IL-1 Receptor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCGGATCCCC TCCTGAGAAG CT

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Primer Oligonucleotide Upstream of
Transmembrane Portion of

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCGGATCCCA TGTGCTACTG G

21

Country	Year	GDP (constant 2005 US\$)		Population (millions)		Urban population (millions)		Rural population (millions)		Total population (millions)	
		1990	2000	1990	2000	1990	2000	1990	2000	1990	2000
Algeria	1990	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2000	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2005	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2010	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2015	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2020	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2025	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2030	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2035	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2040	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2045	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2050	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2055	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2060	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2065	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2070	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2075	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2080	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2085	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2090	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2095	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2100	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2105	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2110	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2115	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2120	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2125	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2130	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2135	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2140	10,000	10,000	10.0	10.0	5.0	5.0	5.0	5.0	10.0	10.0
Algeria	2145	10,000	10,000	10.0	10.0	5.0	5.0	5.0</			